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SEQ ID NO: 6	A33	1	W G K W W P V L W T C A Y R V T Y D A I S V E T P Q D V L R A S S Q G K S V T L P C T Y H T S T S
SEQ ID NO: 1	40628	1	W G T K A Q V E R K L C L F I L A I L C S L A L G S Y T V H S S E . . . . . P E Y A I P E
SEQ ID NO: 2	45416	1	W G I L G L L G L L G H L T Y D T Y G R P I L E V P E S V T G P W K G D V N L P C T Y O P L
SEQ ID NO: 9	35638	1	W A R S R H A L L L R Y L V V A L G Y H K A Y G F S A P K D O . . . . . O V Y T A V E
SEQ ID NO: 10	JAM	1	W G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q . . . . . S D Y Q V P E
A33	51	S R E G L I Q W D K L L L T E R V V I W P F S H K N Y I H G E L Y K N R V S I S H H A E Q S D A	
40628	43	H N P V K L S C A Y S G F S S P R V E W K F D Q G D O T T R L Y C Y N N K I T A S Y E D R V T F L P T	
45416	47	Q G Y T Q V L Y K W L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H Y S H K V P G D V	
35638	43	Y Q E A I L A C K T P K X T V S R L E W K K L G R S V S F Y Y Q Q T L Q G D F K N R A E M I D F	
JAM	42	N E S I K L T C T Y S G F S S P R V E W K F V Q G S T T A L Y C Y N S Q I T A P Y A D R V T F S S S	
A33	101	S I T I D Q L T H A D O N G T Y E C S V S L . W . . . . . S D L E G N T K S R V A L L V L V P P S K	
40628	93	G I T F K S Y T R E D T G T Y T C M V S E . . . . . E G G N S Y G E V K V K L I V L V P P S K	
45416	97	S L Q L S T L E W D O R S H Y T C E V T W Q T P D G N Q V V A D K I T E L R Y Q K L S V S K P T V T	
35638	93	N I R I K N V T R S D A G K Y R C E V S A P S . . . . . E G G A N L E E D T Y T L E V L V A P A V	
JAM	92	G I T F S S Y T R K D N G E Y T C M V S E . . . . . E G G Q H Y G E V S I H L T V L V P P S K	
A33	144	P E C G I E G E T I I G N N I O L T C O S K E G S P T P Q Y S W K R Y N I L N Q E Q . . . . .	
40628	135	P T V N I P S S A T I G N R A Y L T C S E Q D G S P P S E Y T W F K D G I V W P T N . P K S T R A F	
45416	147	T G S G Y G F T V P Q G M R I S L O C O A R . G S P P P I S Y I W Y K Q Q T N N Q E P . . . . .	
35638	137	P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L E N . P R L G S Q S	
JAM	134	P T I S V P S S V T I G N R A Y L T C S E H D G S P P S E Y S W F K D G I S W L T A D A K K T R A F	

FIG.-1A

SEQ ID NO: 6 A33 186 . . . PLA QPAS GQPV S L K N I S T D T S G Y I C T S S N E E G . . . . . T Q F C H N I T V  
 SEQ ID NO: 1 40628 184 S N S S Y V L H P T T G E L Y F D P L S A S D T G E Y S C E A R N G Y G . . . . . T P M T S H A V  
 SEQ ID NO: 2 45416 188 . . . I K V A T L S T L L F K P A V I A D O S G S Y F C T A K G Q V G S E Q H S D I V K F V V K D  
 SEQ ID NO: 9 35638 186 T N S S Y T M N T K T G T L Q F N T V S K L D T G E Y S C E A R N S V G . . . . . Y R R C P G K R  
 SEQ ID NO: 10 JAM 184 W N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C O A Q N G Y G . . . . . T A M R S E A A

A33 227 A Y R S P S W N Y A L Y V G I A V G V V A A L I I I G I I I Y C C C C R G K D D N T E D K E D A . . .  
 40628 228 R H E A V E R N V G Y I V A A V Y I V T L I L L G I L V F G I W F A Y S R G H F D R T K K G T S . . .  
 45416 233 S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W D W T D M D G Y L G E I S A G P G K S L  
 35638 230 . W Q V D D L N I S G I I A A V V V A L V I S V C G L G V C Y A A R K G Y F S K E T S F Q K S . . .  
 JAM 228 H W D A V E L N V G G I V A A V V I V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P . . .

A33 275 . R P N R E A Y E E P P E Q L R E L S R E E E E D D Y R Q E E Q R S T G R E S P D H L D Q  
 40628 275 . . . . . . . . . S K K V I Y S Q P S A R S E E G E F K O T S S F L V . . . . . . . . .  
 45416 283 P V F A I I I I S L C C M V V F T H A Y I W L C R K T S Q Q E H V Y E A R . . . . . . . . .  
 35638 277 . N S S S K A T T W . S E N V Q W L T P V I P A L W K A A A G G S R G Q E F . . . . . . . . .  
 JAM 276 . . . . . . . . . G K K V I Y S Q P S T R S E E G E F K Q T S S F L V . . . . . . . . .

**FIG.-1B**

SEQ ID NO:1

Met	Gly	Thr	Lys	Ala	Gln	Vai	Glu	Arg	Lys	Leu	Cys	Leu	Phe	Ile	Leu	Ala	Ile	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr					
1																	10	15	20	25	30											
Val	His	Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Asn	Pro	Val	Lys	Leu	Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val		
																	35	40	45	50	55	60										
Glu	Trp	Lys	Phe	Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Vai	Cys	Tyr	Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu			
																	65	70	75	80	85	90										
Pro	Thr	Gly	Ile	Thr	Rhe	Lys	Ser	Vai	Thr	Arg	Glu	Asp	Thr	Gly	Thr	Tyr	Thr	Cys	Met	Val	Ser	Glu	Glu	Gly	Asn	Ser	Tyr	Gly				
																	95	100	105	110	115	120										
Glu	Val	Lys	Val	Lys	Ile	Vai	Val	Leu	Pro	Pro	Ser	Lys	Pro	Thr	Vai	Asn	Ile	Pro	Ser	Ser	Ala	Thr	Ile	Gly	Asn	Arg	Ala	Val				
																	125	130	135	140	145	150										
Leu	Thr	Cys	Ser	Glu	Gln	Asp	Gly	Ser	Pro	Pro	Ser	Glu	Tyr	Thr	Trp	phe	Lys	Asp	Gly	Ile	Val	Met	Pro	Thr	Asn	Pro	Lys	Ser	Thr			
																	155	160	165	170	175	180										
Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	Vai	Leu	Asn	Pro	Thr	Thr	Gly	Glu	Leu	Val	phe	Asp	Pro	Leu	Ser	Ala	Ser	Asp	Thr	Gly	Glu	Tyr			
																	185	190	195	200	205	210										
Ser	Cys	Glu	Ala	Arg	Asn	Gly	Tyr	Gly	Thr	Pro	Met	Thr	Ser	Asn	Ala	Vai	Arg	Met	Glu	Ala	Val	Glu	Arg	Asn	Val	Gly	Val	Ile	Val			
																	215	220	225	230	235	240										
Ala	Ala	Vai	Val	Thr	Ile																											
																	245	250	255	260	265	270										
Lys	Gly	Thr	Ser	Ser	Lys	Val	Ile	Tyr	Ser	Gln	Pro	Ser	Ala	Arg	Ser	Glu	Gly	Glu	Phe	Lys	Gln	Thr	Ser	Arg	Gly	His	Phe	Asp	Arg	Thr	Lys	
																	275	280	285	290	295	299										

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**FIG.\_2**

SEQ ID NO:2

1 MGIIICLJJL CHLTVDTYGR PILEVPESVT GPWKGDVNLPL CTYDPLQGYT QVLVVKMLVQR GSDPVTLFLR DSSGDHIIQQA KYQGRLLHVSH KVPGDVSSLQL

101 STLEMDDRSH YTCEVTVWQTPP DGNQQVVRDKI TELRVQKLSV SKPTVTTSG YCFTPQGMR ISLQCQARGG PPISYYIWYKQ QTNNQEPIKV ATLSTLLFKP  
 ^Glycosaminoglycan attachment site

201 AVIADSGSYF CTAKGQVGSE QHSIVKFWV KDSSSKLKKTK TEAPTTMTPP LKATSTVKQS WDWTTDMGY LGETSAGPGK SLPVFATILLI ISLCCMVFT  
Transmembrane domain

301 MAYIMLCKRT SQQEHVYEEAA R

OLI2162 (35936.f1)

SEQ ID NO:12

TCGGGGAGCTGTGTTCTGTTTCCC

OLI2163 (35936.p1)

SEQ ID NO:13

TGATCGCGATGGGGACAAAGGCCAAGCTCGAGAGGAAACTGTTGTGCCT

OLI2164 (35936.f2)

SEQ ID NO:14

ACACCTGGTTCAAAGATGGG

OLI2165 (35936.r1)

SEQ ID NO:15

TAGGAAGAGTTGCTGAAGGCACGG

**FIG.-3**

OLI2166 (35936.f3)

SEQ ID NO:16

TTGCCTTACTCAGGTGCTAC

OLI2167 (35936.r2)

SEQ ID NO:17

ACTCAGCAGTGGTAGGAAAG

**FIG.-8**

DNA35936 SEQ ID NO:3

CTTCTTGCCA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50  
 GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGGAG 100  
 GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150  
 CATCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200  
 AACAAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250  
 GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300  
 TGTCCTGAAT CCCACAAACAG GAGAGCTGGT CTTGATCCC CTGTCAGCCT 350  
 CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

**FIG.\_4A**

consen01 SEQ ID NO:4

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50  
 CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100  
 GCGCAAGCTC GAGAGGAAAC TGTTGTGCCT CTTCATATTG GCGATCCTGT 150  
 TGTGCTCCCT GGCATTGGC AGTGTACAG TTGCACTCTT CTGAACCTGA 200  
 AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCTGT GCCTACTCGG 250  
 GCTTTCTTC TCCCCGTGTG GAGTGGAAAGT TTGACCAAGG AGACACCACC 300  
 AGACTCGTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350  
 GACCTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAAGACA 400  
 CTGGGACATA CACTTGTATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450  
 GAGGTCAAGG TCAAGCTCAT CGTGTGTG CCTCCATCCA AGCCTACAGT 500  
 TAACATCCCC TCCTCTGCCA CCATTGGAA CCGGGCAGTG CTGACATGCT 550  
 CAGAACAAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600  
 ATAGTGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650  
 CTATGTCCTG AATCCACAA CAGGAGAGCT GGTCTTGAT CCCCTGTCAG 700  
 CCTCTGATAAC TGGAGAATAC AGCTGT 726

**FIG.\_4B**

consen02 SEQ ID NO:5

GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50  
 ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100  
 ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150  
 TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCCACAG 200  
 TGACAACCTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250  
 AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTGGT 300  
 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG 350  
 TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTCT 400  
 GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450  
 TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500  
 TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550  
 GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600  
 CCAGGAAAGA GCCTGCCTGT CTTGCCATC ATCCTCATCA TCTCCTTGTG 650  
 CTGTATGGTG GTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700  
 CCCAACAAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750  
 AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800  
 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAACTA CTCTGATGAG 850  
 CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900  
 CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950  
 AGGGCAAAAG TGTCTGTTAA AAATGCCCA TTAGGCCAGG ATCTGCTGAC 1000  
 ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050  
 CTCTCTTCCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT 1100  
 GGGAGTCACT GGCTTGCCC TGGAAATTGC CAGATGCATC TCAAGTAAGC 1150  
 CAGCTGCTGG ATTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200  
 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250  
 TTGGTCATCA TGCCTACAGA CACTATTCAA CTTGGCATC TTGCCACCAG 1300  
 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350  
 CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTAA TTGAAATTGT 1400  
 TATTTCACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450  
 TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500  
 AAA 1503

**FIG.\_4C**

SEQ ID NO:11 GGAGTCCTT CGGGGCTGT TGTGTCAGTG GCCTGATGCC GATGGGACA AAGGCCAAG TCGAGGAA ACTGTTGTGC CTCTTCATAT 100  
 TGGCGATCCT GTGTCCTC CTGGCATGG CGAGTGTAC AGTGCACCT TCTGAACCTG AAGTCAGAAT TCCTGAGAAT AACCCCTGTA AGTTGTCTG 200  
 TGCCTACTCG GGCTTCTCT CTCCCCGTGT GGAGTGGAAAG TTGACCAAG GAGACACCAC CAGACTCGTT TGCTTATAATA ACAAGATCAC AGCTTCCTAT 300  
 GAGGACCGGG TGACCTCTT GCCAACCTGT ATCACCTCA AGTCCGTGAC ACGGGAAGAC ACTGGACAT ACACCTGTAT GGTCTCTGAG GAGGGGGCA 400  
 ACAGCTATGG GGAGGTCAAG GTCAAGCTCA TCGTGCCTGT GCCTCCATCC AGGCTACAG TAAACATCCC CTCCCTGTC ACCATGGGA ACCGGGAGT 500  
 GCTGACATGC TCGAACAAAG ATGCTCCCC ACCTTCTGAA TACACTGGT TCAAAAGATG GATACTGATG CCTACGAATC CAAAAGCAC CCGTGCCTC 600  
 AGCAACTT CCTATGCTT GAATCCACA ACAGGAGAGC TGGTCCTGTA TCCCCTGTC GCCTGAGAATA CAGCTGTGAG GCACGGAATG 700  
 GGTATGGAC ACCCATGACT TCAAATGCTG TCGGCATGGA AGCTGTCAGC CGGAATGTC GGTCATCGT GGCAGCGTC CTGTAACCC TGATTCTCCT 800  
 GGGAAATCTG GTTGTGCA TCTGGTTGC CTATAGCCGA GGCCACTTTC AGAAACAAA GAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCAGCCT 900  
 AGTGCCTGAA GTGAAGGAGA ATTCAACAG ACCTCGTCAT TCCCTGTCAG CTCAGGATG CCTTATTTGT CCCTACACC CCACAGGGCC CCTACTCTT TCGGATGTGT TTAAATAAT 1100  
 ACCGGACTCT GGCCTCTGAT GTCTGTAGTT TCACAGGATG CCTTATTTGT CCCTACACC CCACAGGGCC CCTACTCTT TCGGATGTGT TTAAATAAT 1100  
 GTCAGCTATG TGCCTCATCC TCCCTCATGC CCTCCCTCCC TTCCATACCA CTGCTGAGTG GCCTGGAACT TGTAAAGT GTTAAAGT GTTAAAGT GTTAAAGT 1200  
 AGGGATCAGG AGGAATCTT GGGTATGCC TTGACTTCCC TTCTAAGTAG ACAGCAAAA TGGGGGGT CCCAGGAATC TGCACCTAAC TGCCACCTG 1300  
 GCTGGAGGG ATCTTGAAT AGGTATCTG AGCTGGTC TGGCTCTT CCTGCTGTAC TGACGACAG GGCAGCTGT TCTAGAGGG GAATTAGAGG 1400  
 CTAGAGGGC TGAATGGTT GTTGTGAT GACACTGGG TCCCTCCATC TCTGGGGCC ACTCTCTT GTCTTCCAT GGGAAATGCC ACTGGGATCC 1500  
 CTCCTGCCTG TCCCTCTGAA TACAAGCTGA CTGACATTGA CTGCTGTGT GAAATGGG AGCTCTTGT GTGGAGAGCA TAGTAAATT TCAGAGAACT 1600  
 TGAAGCCAAA AGGATTTAA ACCGGCTGCTC TAAAGAAAG AAAACTGGG GCTGGCTACG CCTGTAATC CAGAGGCTGA GCGAGGGCA 1700  
 TCACTGAGG TCGGGAGTT GGGATCAGCC TGACCAACAT GGAGAAACCC TACTGGAAAT ACAAGTTAG CCAGGATG TGTTGCATGC TTGTTGCCTCC 1800  
 AGCTGCTCAG GAGCCTGGCA ACAAGGAGCA AACTCCAGGT CA 1842

FIG.-5

SEQ ID NO:7

1 CCCACCCCTC CGCCCCACGGG TCCCCCACCG GCTCCCCCA CGCCTCCGGG CCACCAAGAG TTTCGCTCC CTTGGCTACCA GGAGGGTCCA AGAAACGCA  
GGGGGGCCAG GGGGGGGCCAG AGGGGGTCCAG GGGGGGGCT GGGGGGGCT AAGCTCGGA AAACCTCGGT CCTTCGACCT TCTTTCCTGT

101 GAACTAGCTC TGGCTGTGAT GGGCATCTTA CTGGGGCTGC TACTCTGGG GCACCTAACAA GTGGACACTT ATGGCCGCTCC CATCCCTCAA GTGCCACAGA  
CTTCATCGAG ACCGACACTA CCCCTAGAAT GACCCGGACG ATGAGGACCC CGTGGATTGT CACCTGTGAA TACCGGAGG GTAGGACCTT CACGGTCTCT

1 SEQ ID NO:2 M G I L L G L L L C H L T V D T Y G R P I L E V P E S  
^MET

201 CTCGACAGG ACCTTGAAA GGGCATGTCATGAC ATCTTCCCTG CACCTATGAC CCCCTCCAAAG CCTACACCCA ACTCTTGGTC AACCTGGTGG TACAACGTCG  
CACATTCCTC TGGAAACCTTT CCCCTACACT TAGAACGGAC GTGGATACCTG GGGGACCTTC CGATCTGGCT TCAGAACCCAC TTCAACGGACC ATGTTGGACCC

29 V T C P W K G D V N L P C T Y D P L Q C Y T Q V L V K W L V Q R G

301 CTCAGACCCCT CTCACCATCT TTCTAAGTGA CTCCTCTGGA GACCATATCC ACCAGCCAAA GTACCAAGGGC CGCTGTGATG TGAGCCACAA GGTTCCAGGA  
GAGCTGGGA CAGTGGTAGA AAGATGCACT GAGAAAGACCT CTGGCTATAGG TCGCTCCGGT CATGGTCCC GGGGACTGTAC ACTGGTGTCTT CCAAGGTCTT  
62 S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P C

401 GATGTATCCC TCCAATTGAG CACCTGGAG ATCGATGACCC GGAGCCACTA CACGTGTGAA GTCACCTGGC AGACTCTGA TCCCACACAA GTCGTGAGAG  
CTACATACCC ACCGTAACCTC GTGGGACCTC TACCTACTGG CCTCTGGTGTAT GTGCAACACTT CAGTGGACCC TCTGAGGACT ACCGTTGGTT CAGCACTCTC

95 D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D

501 ATAAGATTAC TGAGCTCCGT GTCCAGAAAC TCTCTGCTC CAAGCCCCACA GTGACAACTG GCAGGGTTA TGGCTTCAGG GTCCCCCAGG GAATGACCAT  
TATTCTAATG ACTCGAGGA CAGCTCTTG AGACACAGAG GTTCGGGGTGT CACTGTGAC GTGCGCCAAT ACCGAAAGTGC CACGGGCTC CTTACTCTCA

129 K I T E L R V Q K L S V S K P T V T C S C Y G F T V P Q G M R I

601 TAGCCTCAA TGCCAGGGCTC GGGGTTCTCC TCCCATCACT TATATTTGGT ATAAGCAACA GACTAATAAC CAGGAACCA TCAAAAGTAGG AACCCCTAAGT  
ATCGGAAGTT ACGGTCCGAG CCCCAAGAGG AGGGTAGTCA ATATAAACCA TATTCTGGTGT CTGATTATTG GTCCTTGGGT AGTTTCATCG TTGGGGATTCA

162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

FIG.-6A

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SEQ ID NO:7 701 ACCTTACTCT TCAAGCCTGC GGTGATGCC GACTCGGCT CCTATTCTG CACTGCCAAG GCCCACGGTG GCTCTGAGCA GCACAGGAC ATTGTGAAGT  
TCCAATGAGA AGTTCGGAGC CCACTATCGG CTGAGTCCGA CGNATAAGAC GTGACGGTT CCGGTCNAAC CGAGACTCGT CGTGTGCTG TAACACTTCA  
SEQ ID NO:2 195 T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F

801 TTGTCGTCAA AGACTCCTCA AGACTACTCA AGACCAAGAC TGACCCACCT ACAACCATCA CATACCCCTT GAAACCAACA TCTACAGTGA AGCAGTCCTG  
AACACCACCT TCTCAGGACT TTGATGAGT TCTGGCTCTG ACTTCGGTGA TCTTCGTTACT CTATGGAA CTTCGGTGT AGATGTCACT TCCTCAGGAC  
229 V V K D S S K L L K T K T E A P T M T Y P L K A T S T V K Q S W

901 GGACTGGACC ACTCACATGG ATGGCTTACCT TGGAGNACCC AGTGGCTGGGC CAGGNNAGC CTCGCCCTGTC TTTGCCATCA TCCTCATCAT CTCCCTGCTG  
CCTGACCCCTGG TGACTGTACCC TACCGATGGA ACCTCTCTGG TCACGACCCGG CCTCCCTTCTC GGACCCACAG AACCGTAGT AGGAGTAGTA GAGGAACACG  
262 D W T T D M G Y L G E T S A G P K S L P V F A I I L I I S L C

1001 TCTATGGTGG TTTTACCAT GGCCTATATC ATGCTCTGTC CGAACACATC CCAACNAGC CATGCTTACG AGGAGCCAG CTAAAGAACT CTCTCCTCTT  
ACATACACC AAAATGTA CGGGATATAC TACGAGATAG CCTTCTCTAG GGTTCTCTTC CTACAGATGC TTCTGCTGGTC CATTCTTCA GAGGAGGAA  
295 C H V V F T M A Y I M L C R K T S Q Q E H V Y E A A R O

1101 CCATTTTGA CCCCTCCCT CCCCTCAATT TTGATTACTG GGAGGAAATG TGGAGGAAGG GGGTGTGGC ACAGACCCAA TCCTAAGGGC CGAAGGCTTC  
GGTAAAACCT GGGCAGGGA CGGGCAGGAA AACTATGAC CGTCTCTTAC ACCTCCTTC ACCTCCATCTG TCTCTGGCT AGGATTCCCG CCTCCGGAAAG

1201 AGGGTCAAGA CATAGCTGCC TTCCCTCTT CAGGCCACCTT CTGAGGTGT TTTGGCCCTC TGACACAM CGATAATTAA GATCCATCTG CCTTCTGCTT  
TCCCAGTCT GTATGGACCG AAGGGAGAGA GTCCGTGGAA GACTCCAAACA AACCCGGAG ACTTGTGTT CCTATTAAAT CTAGGTAGAC CGTTCAGGAA AGAATACCAA  
GGTCTTGGG ACCCACCATC CTAGGACTAT TAATAACCG TTCTTAACTC CGTCTTCCCA CCCTTGGTC CTGGTGTGG CGTTCAGGAA AGAATACCAA

1301 CCAGAATCCC TGGGGTAG GATCCCTGATA ATTAAATCGG AAGAATGAG GCAGAAGGT GGGAAACAG GACCAAGCC CCAAGTCCCT TCTTATGGT  
CCACCCGAGA ACCCGTATC CGGTGACCG TCTCTCGGT TCTCTGAGACC TCTTGGTAC TCCCTGGT AGAACGGTT ACGGACAGGG TCACATCTCG

1401 GGTGGCTCT TGGGCCATAG GGCACATGCC AGAGAGGCC ACCACTCTGG AGAACCTAG AGGGGGCA TCTTCCAG TGGCTGCTCC ACTGATGAGC  
CCACCCGAGA ACCCGTATC CGGTGACCG TCTCTCGGT TCTCTGAGACC TCTTGGTAC TCCCTGGT AGAACGGTT ACGGACAGGG TCACATCTCG

1501 CAACTCCCA GAATCTGGEC ACAACTACT CTGATAGGCC CTGCTATAGGA CAGGAGTAC AGATCATCGC CGAGATCAAT CGCAACTACG CCCGCTTGT  
CTTGAAGGGT CTTAGACCCG TTGTTGATGA GACTACTCGG TCTAGTACGG TCTAGTACGG CGTCTAGTA CGTGTGATGC CGGTCAAGGA GGGGGACGA

FIG.-6B

SEQ ID NO:7

1601 CGACACACTT CCTCTGGATT ATGACTTCTT CCTCACTGAG CCCACACTGAG TCTCTTAAAT ATGCCCCATTT AGCCAGGAT CTCCTGACAT AATTGCCCTAG CCTCTGTCAA CGAGACCTAA TACTCAAAAG CCCTGTACTC CCCTTTCAC AGACAAATTT TACCCCCCTAA TCCGGTCTTA GACGACTGTA TTAAACGGATC

1701 TCAGTCCTTG CCTTCCTGCAT CCCCTTCTTC CCTGCTTACCT CTCTCTCTGG ATAGCCCCAAA GTGTCGGCTT ACCAACACTG GACCCGGCTGG GAGTCACCTGG ACTCTAGGAAC CGAAGACCTA CGGGAAAG CGAGGATGCA GAGAAGGACC TATCGGGTTT CACACCCCCAA TGCTTGTGAC CTGGGGGACCTCAGTGAAC

1801 CTTTGCCTTG GAATTGGCCA GATGGCATCTC AAGTAAGCCA GCTGCTGGAT TTGGCTCTGG GCCCTTCTAG TATCTCTGCC EGGGGCTTCT GGTAACCTCTC GAAAGGGCAC CTTAAACGGT CTACGTAGAG TTCAATTGGGT CGACGACCTA AACCGAGACC CGGAAGACATC ATAGAGACGG CCCGGAAAGA CCATGACAG

1901 TCTAAATACC AGACCCAAAGA TCCCCATAGC ACTAGGACTT CCTACAGACA CTATTCACACT TTGGCATCTT CCCACCAAGAA GACCCGAGGG AGATTTATCC TCTCCCTTCT ACGGGTATCG TGMTCCTGAA CCAGTAGTAC CGATGCTCTGT GATAAGTGA AACCGTAGAA CGGGGGCTTCTT CTGGGGCTCCC

2001 AGGGCTCAGCT CTGCCAGCTC AGAGGACCCAG CTATATCCAG GATCATTCTC CTTTCTTCAG GCCCAGACAG CTTTTAATTG AATTGTTAT TTCACAGGGCC TCCCCAGTCAA GACGGTCCAG TCTCCTGGTC GATATAGCTC CTACTAAAGA GAAGGAAGTC CGGGTCTGTC CAAATAAC TTAAACATA AAAGTGTCCGG

2101 AGGGTTCACT TCTGCTCCTC CACTATAACT CTMATTCTCT GACTCTCTCC TGGTCTCMA TAAATATCTA ATCATACAG C TCCCCAAGTCA AGACGGAGG C TGTGATTTCA GATTACAGCA CTGAGAGGG ACCACGGAGTT ATTATAGAT TACTATGTC G

**FIG.-6C**

SEQ ID NO:8

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGACCCCTGACCTCCT  
 CAGAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGCAGGAGCCACC GCCCTCCTCCT  
 GCTGCTGCTGCCCTACCTGGTGGTCGCCCTGGCTATCAT AAGGCCTATGGGTTTCTGC  
 CCCAAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAA  
 AACCCCAAAGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTC  
 CTTGTCTACTATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGA  
 TTTCAATATCCGGATCAAAAATGTGACAAGAAGTGTGAGTGCAGGGAAATATCGTTGTGAAGT  
 TAGTGCCCCATCTGAGCAAGGCCAAACCTGGAAGAGGATACTGACTCTGGAAGTATT  
 AGTGGCTCCAGCAGTCCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGT  
 AGAGCTACGATGTCAAGACAAAGAAGGGAACTCAGCTCCTGAATAACACATGGTTAAGGA  
 TGGCATCCGTTGCTAGAAAATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACAC  
 AATGAATAACAAAATGGAACTCTGCAATTAACTGTTCCAAACTGGACACTGGAGA  
 ATATTCCGTGAAGCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGAAACGAATGCA  
 AGTAGATGATCTAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTAGTGAT  
 TTCCGTTGTGGCCTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTCAAAAGAAAC  
 CTCCCTCCAGAAGAGTAATTCTCATCTAAAGCCACGACAATGAGTAAAATGTGCAGTG  
 GCTCACGCCTGTAATCCCAGCACTTGGAAAGGCCGCGGGGGATCACGAGGTCAGGA  
 GTTCTAGACCAGTCTGGCCAATATGGTAAACCCCATCTACTAAAATACAAAAATTAG  
 CTGGGCATGGTGGCATGTGCCTGCAGTCCAGCTGCTGGAGACAGGAGAATCACTTGA  
 ACCCGGGAGGCAGGTTGCAGTGAAGATCACGCCACTGCAGTCCAGCCTGGGTAA  
 CAGAGCAAGATTCCATCTAAAAATAAAATAAAATAACTGGTTTAC  
 TGTAGAATTCTTACAATAATAGCTTGATATT

**FIG.\_7**

SEQ ID NO:9

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT  
 LEWKKLGRSVSFVYYQQLQGDKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQN  
 LEEDTVTLEVVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWF  
 KDGIRLLENPR  
 LGSQSTNSSYTMNTKTGTLQFNTVSKLDGEYSCEARN  
 SVGYRRCPGKRMQVDDLNISGI  
 IAAVVVVALVISVCGLGV  
 CYAQRKGYFSKETSFQKSNSSSKATTMSENV  
 QWLTPV  
 IPALW  
 KAAAGGSRGQEF

**FIG.\_11**

SEQ ID NO:5

1 CGAGGAAAG TACCCAGGGCC CCCTGCATGT GAGCCACMAG GTTCAGGGAG ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GACCCACTAC  
CCTCCGTTTC ATGGTCCCCG CGGACGTACA CTCCGCTCTC CAGGCTCCTC TACATAGGA CGTTAATCTG TGGACCTCT ACCTACTGGC CTCGGTGATG  
^42257 . f1 SEQ ID NO:18 ^42257 . p1 SEQ ID NO:22

101 ACGTGTGAGG TCACCTGGCA GACTCCTGAT GGCAACCAAAG TCGTAGAGA TAAGATTACT GAGCTCGTG TCCAGAACT CTCAGTCTCC AACCCACAG  
TGCACACTTC AGTGGACCGT CTGAGGACTA CCCTGGTTCA ACCACTCTCT ATTCTTAATGA CTTCAGGAC AGGTCTTTGA GAGACAGGG TTGGGTGTC  
^42257 . r1 SEQ ID NO:18

201 TGACAACTGG CAGGGTTAT GGCTTCACGG TGGCCACGG AAAGGAGGTT AGCCTTCAT CCCAGGGTTCC CGGTTCTCC TCCCATCAGT TATATTGGT  
ACTGTGTGAC CTGGCCAATA CGGAAGTGGC AGGGGTCTCC TTACTCCTAA TCCGAACTTA CGGTCCAAG CCCAAAGGG AGGGTAGTC ATATAAACCA

301 ATAAGGAACA GACTAATAAC CAGGAAACCC ATCAAAAGTAG CAACCCCTAAC TAGCTTACTC TTCAACCCCTG CGGTGATACC CGACTCAGGC TCCTATTCT  
TATTGTTGT CTGATTATTC CTCCCTGGC TACTTCATC GTGGGATTC ATGGAATGAC AAGTTGGAC GCCACTATCG GCTGAGTCC AGGATAANGA

401 GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTCAGG TTTGTCAGTCA AAGACTCTC AAAGCTACTC AAGACCAAGA CTGAGGGACC  
CGTGACGGCTT CCCGGTCCAA CGGAGACTCG TGCTGTGCTG GTAAAGCTTC AAACCACTG TTCTGAGGAG TTCTGATGAG TTCTGGTTCT GACTCGTGC  
^42257 . r1 SEQ ID NO:20

501 TACAACCATG ACATAACCCCT TGAAGGAAAC ATCTACAGTG AAGGAGCTCT GGACTGGC CACTGACATG GATGGCTTACG TTGGAGAGAC CAGTCCTGG  
ATGTTGGTAC TGATGGGA ACTTTCGTTG TAGATGTCAC TTCCGTCAGGA CCTGACCTG GTGACTGTAC CTACCGATGG AACCTCTCTG GTCACCAACC  
^42257 . r1 SEQ ID NO:20

601 CAGGAAAGA GCCTGCCCTGT CTTTGCCATC ATCCCTCATCA TCTCTCTGCTG CTGATGGT GTTTTACCA TGGCTCTAT CATGGCTCTGT CGGAGACAT  
GTCCTTCTC CGGACGGACA GAAACGGACA TAGGAGTAAGT AGAGGAACAC GACATACAC CAAAAATGGT ACCGGATATA GTACCGAGACA GCCTTCTGTA  
^42257 . f2 SEQ ID NO:19

701 CCCAACAAAGA CCATGCTTAC GAAACGGCCA GGGCACATGC CAGAGGGCC AACGACTCTG GAGAACCAT GACCGTGGCC ATCTTCGCAA GTGGCTGCTC  
GGTTGGTTCT CGTACAGATG CTTCGTCGGT CCCGTGTAAGC GTCTCTCCGG TTGCTGAGAC CTCCACCGG TAGAAGGCTT CACCGACGAG

FIG.- 9A

SEQ ID NO:5

801 CAGTGATGAG CCAAACCTCCC AGAATCTGGG GCMCAACTA CTCTGATGAG CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA  
GTCACTACTC GGTTGAAGGG TCTTAGACCC CGTGTGAT GAGACTACTC GGGACGTATC CTGTCCTCAT GGTCTAGTAG CGGCTCTAGT TACCGTTGAT

901 CGCCCCCTG CTGGACACAG TTCTCTGGA TTATGAGTTT CTGGCCACTG AGGGCAAAAG TGTCCTGTTAA AAATGCCCA TTAGGCCAGG ATCTGCTGAC  
GGGGGGGAC GACCTGTGTC AAGGAGACTT AATACTAAA GACCGGTGAC TCCCCTTTC ACAGACAATT TTACGGGT AATCCGGTC TAGACGACTG

1001 ATAATGGCT AGTCAGTCCT TGCCTCTGC ATGGCCCTCT TCCCTGCTAC CTCTCTTCTC CGATAGCCC AAATGCCCA CTACAAACAC TTGAGCCCT  
TATTAACGGA TCACTCAGGA ACGGAAGACG TACCGGAAAGA AGGGACGATG GAGAGAAGGA CCTATCGGGT TTCACAGGG GATGGTGTG ACCTCGGGCA

1101 GGGAGTCAT GGTGTTGCC CGGAAATTGC CAGATGCCATC TCAAGTAAAC CAGCTCTGG ATTGGCTCT GGGCCCTCT AGTATCTCTG CGGGGGCTT  
CCCTCACTGA CGGAAACGGG ACCTTAACAG GTCTACGTTAG AGTTCTATTG CTCGACGACC TAACCGGAA TCATAGAGAC GGGGGGGAA  
^42257.r2 SEQ ID NO:21

1201 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGGCCATA GCACTAGGAC TTGGTCATCA TGCTCTACAGA CACTATTCA CTTGGCCTAC TTGCCCACCAAG  
GACCATGAGG AGAGATTAT GGTCTCCCTT CTACGGCTAT CGTGATCTG AACCACTAGT ACCGATGTT GTGATAAGTT GAAACCGTAG AACCGTGGC

1301 AAGACCCGAG GGGAGGCTCA GGTCTGCCAG CTCAAGGGAC CAGCTATTC CAGGATCATT TCTCTTTCTT CAGGGCAGA CAGCTTTAA TTGAAATTGT  
TTCTGGGCTC CCCTCCGAGT CGAGACGGTC GAGTCTCTG GTGGATATAG GTCCTAGAA AGAGAAAGAA GTCCGAATT AACTTAACAA

1401 TATTACACAG CCAGGGCTTC AGTTCTGCTC CTCACACTATA AGTCTAATGT TCTGACTCTC TCCTGGGTCT CAATAATAT CTAACTAA CAGCAAAAAA  
ATAAAGTGTGTC CGGTCCCAAG TCAAGACGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACCAAGA GTCCTTTTTT GTCCTTTTTT

1501 AAA  
TTT

FIG.\_ 9B

		FRAME	SCORE	MATCH	PCT
A33_HUMAN	A33 ANTIGEN PRECURSOR - HOMO SAPIENS	+1	246	81	30

A33\_HUMAN - A33 ANTIGEN PRECURSOR - HOMO SAPIENS (319 aa)

SCORE = 246 (86.6 BITS), EXPECT = 2.8e-19, P = 2.8e-19

IDENTITIES = 81/268 (30%), POSITIVES = 131/268 (48%), AT 121,17, FRAME = +1

DNA40628 121 LALGSVTVHSSEPEVRIPENNPVKLSAYSFGSSPR---VEM-KFDQGDTTRLV C--YNN

SEQ ID NO:23

A33\_human 17 VTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKL LLTTERVVIWPF SN

SEQ ID NO:24

DNA40628 283 K--ITAS-YEDRVTEFL-----PTGITEFKSVTREDTGTYYTCMV S---E EGGNSYGEVKVK

A33\_human 77 KNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNT-KSRVR

DNA40628 427 LIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGI VMPTNPKSTRAFSN

A33\_human 135 LLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNINLQEQP-----

DNA40628 607 SSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVG V---IVA

A33\_human 187 ---LAQPASGQPVSLKNISTDTSGYI CTSSNEEGTQFCNITVAVRSPSMNVALYVGIAV

DNA40628 775 AVLVTLLGILVFGIWFAYSRGHFDRT-KKGTSKKVIVSQP

A33\_human 244 GVVAALIIIGIIY---CCCCRGKDDNTEDKEDARPNEAYEEP

**FIG.- 10A**

**SCORE = 245 (86.2 BITS), EXPECT = 3.6e-19, P = 3.6e-19  
IDENTITIES = 83/273 (30%), POSITIVES = 131/273 (47%), AT 112,12, FRAME = +1**

DNA40628	112	LCSL--ALGSVTVHSSEPEVRIPENNPKVLSCAYSGFSSPR---VEW-KFDQGDTTRLVC
SEQ ID NO:25	*	*
A33 Human	12	LCAVRVTVDIAISVETPQDVLRASQGKSVTLRPTYHTTSSSREGLIQWDKLLLTHTERVVVI
SEQ ID NO:26	*	*

DNA4 0628 274 - YNNK--ITAS-YEDRVTFL-----PTGITFKSSVTVREDTGTYTCMVSEEGNNSYGEVK  
 A33 Human 72 WPFESNKWYIHINGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMS-DLEGNTK

DNA4 0628 421 -VKLIVLVPPIKPTVNIPSSATIGNRAVLTCEQDGSPPEYTWFKDGIUMPTNPKSTR  
           \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* .

DNA4 131 SFRVLLVYIYPPSKPECGIEGETIIGNNIOLTCOSKEGSPTPQYSWKRYNINLQEOP----

DNA4 0628 595 AFNSSSYVLNPTTGEV-FDPLSASDTGEYSCEARNGYGTPTMSNAVRMEAVERNVGV--  
A33 Human 187 -----LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALVV  
\* \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* . \* .

DNA40628	766	-IVAAVLVTLLILLGILVFGIWFAYSRGHFDRT--KKGTSSKKVIYSQP
	*	* . * * . * * . .
A33	human	240 GIAVGVVAA <del>LIIIGIIY</del> --CCCCRGKDDNTEDKEDARPNEAYEEP

**FIG. 10B**

SEQID NO: 6 A33\_hum 1 ..... M V G K W W P V L W T C A V A R V T V D A I S V E T P O O V L R A S Q Q K S Y T L  
 SEQID NO: 1 40628 1 W G T K A Q V E R K L L C L F I L A I L L C S . . L A L G S V T Y H S S E P E V A R I P E N N P Y K L

A33\_hum 42 P C T Y H T S T S S R E G L I O W D K L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I  
 40628 49 S C A Y S G F S S P R . . . V E W . K F D O G D T T R L V C . . Y N N K . . I T A S . Y E D R V T F

A33\_hum 92 S N N A E Q S D A S S I T I D Q L T W A D N G T Y E C S V S L M S D L E G N T K S R V A R L Y L V P P  
 40628 90 . . . . L P T G I T F K S V I T R E D T G T Y T C H V S E E G G . N S Y G E V K Y K L I Y L V P P

A33\_hum 142 S K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I I L N Q E Q P . . . .  
 40628 133 S K P T V N I P S S A T I G N R A V L T C S E O D G S P P S E Y T W F K D G U V M P T N P K S T R A

A33\_hum 187 . . . . L A O P A S G Q P V S L K N I S T D T S G Y Y I C T S S N N E E G T Q F C N I T V A V R S  
 40628 183 F S N S S S Y V L N P T G E . L V F D P L S A S D T G E Y S C E A R N G Y G T P M T S N A V R M E A

A33\_hum 231 P S M N V A L Y V G I A V G V V A A L I I G I I Y C C . C C R G K D D N T E D K E D A R P N R E  
 40628 232 V E R N V G V . . . I V A A V L V T L I I L G I L V F G I W F A Y S R A G H F D R T K K G T S S K K V

A33\_hum 280 A Y E E P P E Q L R E L S R E E E D D Y R Q E E Q R S T G R E S P D H L D Q  
 40628 279 I Y S O P S A R S E G E F K O T S S F L V

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SEQ ID NO: 6 A33\_hum 1 M V G K W W P V L W T L C A V R V T V D A I S V E T P A D V L R A S Q G K S V T L P C T Y H T S T S  
 SEQ ID NO: 2 45416 1 . M G I L L G L L L G H L T V D T Y G R P I L E V P E S V T G P W K G . D V N L P C T Y D P L Q G

A33\_hum 51 S R E G L I O W D O K L L L T H T E R V V I W . P F S N K N Y I H G E L Y K N R V S I S N N A E Q S D  
 45416 49 Y T Q V L V K W . L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V . P G D

A33\_hum 100 A S I T I D Q L T M A D N G T Y E C S V S . L W S D L E G N T K S A V . . . . . R U L Y L V P P S  
 45416 96 V S L Q L S T L E M D D O R S H Y T C E V T W Q T P D G N O V V R D K I T E L R V Q K L S V S K P T V

A33\_hum 143 K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K R Y N I L N Q E Q P L A Q P A S  
 45416 146 T T G S G Y G F T V P Q G M R I S L o C A A R . G S P P I S Y - W . Y K Q Q T N N Q E P I K V A T

A33\_hum 193 G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T . Q F C N I . T V A V V A S P S M N V A L Y V G  
 45416 193 L S T L L F K P A V I A D S G S Y F C T A X G Q V G S E O H S D I V K F V V K D S S K L L K T K T E

A33\_hum 241 I A V G V V A A I I I G I I I Y C C C C R G K D D O N T E D K E D A R P N R E A Y E E P P E Q L R E  
 45416 243 A P T T W T Y P L K A T S T V K Q S W D W T T D W D G Y L G E T S A G P G X S L P V F A I I I S

A33\_hum 291 L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q  
 45416 293 L C C M V V F T M A Y I M L C A K T S Q Q E H V Y E A R

FIG.-13

SEQ ID NO: 6 A33\_hum 1 . . . W V G K M W P V [WT] C A V R Y T V D . . . A I S V E T P Q D V L R A S O G K S V T L P C  
 SEQ ID NO: 9 35638 1 M A R R S A H R L L L R Y L V V A L G Y H K A Y G F S A P K D Q Q V V T A V E Y Q E A I L A C

A33\_hum 44 T Y H T S T S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N  
 35638 51 . . K T P K K T V S S R L E W K K L . . . G R S V S F V Y Y Q Q T . L Q G D . F K N R . . . .

A33\_hum 94 N A E Q S D A S I T I D O L T M A D N G T Y E C S S I L M S D O L E G N . T K S R V R A L V L V P P S  
 35638 87 . A E N I D F N I R I K N V T R S D A G K Y R C E V S A P S E Q G A N L E E D T V T L E V L V A P A

A33\_hum 143 K P E C G I E G E T I I G N N I Q L T C O S K E G S P T P O Y S W K R Y N I L N O E Q P L A Q P A S  
 35638 136 V P S C E V P S S A L S G T V V E L R A C Q D E G N P A P E Y T W F K D G I R L L E N P R L G S O S

A33\_hum 193 G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T Q F C N I T V A V . . . R S P S M N V A L Y V  
 35638 186 T N S S Y T M N T K T G I L Q F N T . V S K L D T G E Y S C E A R N S V G Y R A C P G K R M Q V D D

A33\_hum 240 G I A V G Y V A L I I G I I I Y C C . . . C C A R G K D D N T E D K E D A R P N R E A Y E E P P E  
 35638 235 L N I S G I I A V V V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S N S S S K A T T

A33\_hum 287 Q L R E L S R . E R E E E D D Y R Q E E Q R S T G R E S P D H L D O  
 35638 285 W S E N V Q O W L T P V I P A L W K A A A G G S R G O E F

SEQ ID NO: 10 jam 1 W G T E G K A G R K L L F L F T . S M I L C G S L V Q G K G S Y Y T A Q S D Y Q V P E N E S I K L R C  
SEQ ID NO: 1 40628 1 W G T K A Q V E R K L L C I L A I I L C S L A L G S V T Y H S S E P E V R I P E N N P V K L S C

jam 50 T Y S G F S S P R V E W K F V O G S T T A L V C Y N S O I T A P Y A D R V T F S S S G I T F S S V T  
40628 51 A Y S G F S S P R V E W K F D Q G D T T R L V C Y N N K I T A S Y E D D R V T F L P T G I T F K S V T

jam 100 R X D N G E Y T C M V S E E G G O N Y G E V S I H L T V L V P P S K P T I S V P S S V T I G N R A V  
40628 101 R E D T G T Y T C M V S E E G G N S Y G E V K V K L I V L V P P S K P T V N I P S S A T I G N R A V

jam 150 L T C S E H D G S P P S E Y S W F K D G I S M U L T A D A K K T R A F H N S S F T I D P K S G O L I F  
40628 151 L T C S E D G S P P S E Y T W F K D G I . V M P T N P K S T R A F S N S S Y V L N P T T G E L V E

jam 200 D P V T A F D S G E Y C Q A Q N G Y G T A H R S E A A H M D A V E L N V G C I V A A V L V T L I L  
40628 200 D P L S A S D T G E Y S C E A R N G Y G T P M T S N A V R M E A V E R N V G V I V A A V L V T L I L

jam 250 L G I L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S O P S T A S E G E F K Q T S S F L  
40628 250 L G I L V F G I W F A Y S R G H F D R T K K G T . S S K K V I Y S O P S A R S E G E F K Q T S S F L

jam 300 V  
40628 299 V

jam	49	C T Y S . . . C F S S P R V E W K F V Q G S T T A L Y . . . C Y N S O I . T A P Y A D R V T F S .
45416	41	C T Y D P L Q G Y T Q V L Y K W L V O R G S D P V T I F L R D S S G O H I Q Q A K Y Q G R L H V S H

jam	90	... .SSG!TFSYTAKDNGEYTCWV...SEE <del>G</del> ONYGEVSIHLTYLVPP
45416	91	KVPGOVSLOLSTLEMDASHYTCEV <del>T</del> WQTPDGNCVROKITELAYOKLSV

jam	132	SKPT	ISVPS	...	SYTIGNRAYLTCSEHDDGSPP	SEYSWFKDGISMLTADA
45446	141	SKPT	VTTG	SCYGF	TYPQGMRISSLOCAR.	SYIWYKOOTN..NOEP

jam	228	H . . . H D A V E L N V G G I V A A V L V T I L G L L I F G . . . V W F A Y S R A G Y F E T T K K
	45416	227 K F V V K D S S K U L K T K T E A P T T M T Y P L X A T S T V K O S S W D W T T D W D G Y L G E T S A

jam 272 G T A P G K K V I Y S S O P S T R S E G E F K Q T S S F L Y  
45416 277 G P G K S L P V F A I L I S L C C M V V F T W A Y I M L C R A K T S Q Q E H V Y E A R

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SEQ ID NO: 10	jam	1	W G T E G K A G R K L L F L F T S H I L G S L V Q G K G S V Y T A Q S D V A V . . . P E N E S I K L
SEQ ID NO: 29	35638	1	W A R R S R H A L L L L L R Y L V V A L G Y H K A Y G F S A P X D Q Q V U T A V E Y Q E A I L
jam	48	T C . T Y S G F S S S P R V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G J T F S	
35638	49	A C K T P K K T V S S R L E W K K L . G R A S V S F Y Y Q Q T L Q G D F K N R A E M I D F N I R I K	
jam	97	S V T R K D N G E Y T C W V S . . E E G G A N Y G E V S I H L T R V L V P P S K P T I S V P S S V T I	
35638	98	N V T A S D A G K Y R A C E V S A P S E Q G Q N L E E D T V T L E V L V A P A V P S C E V P S S A L S	
jam	145	G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F M N S S F T I D P K S	
35638	148	G T V V E L R A C O D K E G N P A P E Y T W F K D G I R L L . E N P R I G S Q S T N S S Y T M N T K T	
jam	195	G O L I F D P Y T A F D S G E Y Y C O A O N G Y C I T A M R S E A A H M D A V E L N V G G I V A A V L	
35638	197	G T L O F N T V S K L D T G E Y S C E A R N S V G . Y A R C P G K R M O V D D O L N I S G I I A A V V	
jam	245	V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S O P S T R A S E G E F K Q	
35638	246	V V A L V I S V C G G I G Y C Y A Q R K G Y F . . . S K E T S F Q K S N S S S S K A T T M S E N V Q O W L	
jam	295	T S S F L V	
35638	293	T P V I P A L W K A A A G G S A G Q E F	

FIG.- 17

SEQ ID NO: 6 A33\_hum 1 . . . . . W V G K W P V L W T . L C A V R V T V D A I S V E T P O D V L R A S Q G K S V T L P C T  
SEQ ID NO: 10 jam 1 W G T E G K A G R K L L F L F T S M I L G S L V Q G X G S V Y T A Q S D V Q V P E N E S I K L L T C T

A33\_hum 45 Y H T S T S S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N A V S I S N N  
jam 51 Y S G F S S P R . . . . V E W . K F V Q G S T T A L V C . . Y N S Q . . I T A P . Y A D R V T F S S .

A33\_hum 95 A E Q S D A S I T I D Q L T W A D O N G T Y E C S V S L W S D O L E G N T K S R V R A L L V L V P P S K P  
jam 91 . . . . S G I T F S S V T R K D O N G E Y T C H V S E E G G . Q N Y G E V S I H L T V L V P P S K P

A33\_hum 145 E C G I E G E T I I G N N I O L T C O S K E G S P T P Q Y S W K R Y N I L N O E Q P L A Q P A S G Q  
jam 135 T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K X T R A F H

A33\_hum 195 P V S L K N I S T D T S G Y Y I C T S N E E G T O F C N . . . . I T V A V R S P S M N . . . . V A L  
jam 185 N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A M R S E A A H M D A Y E L

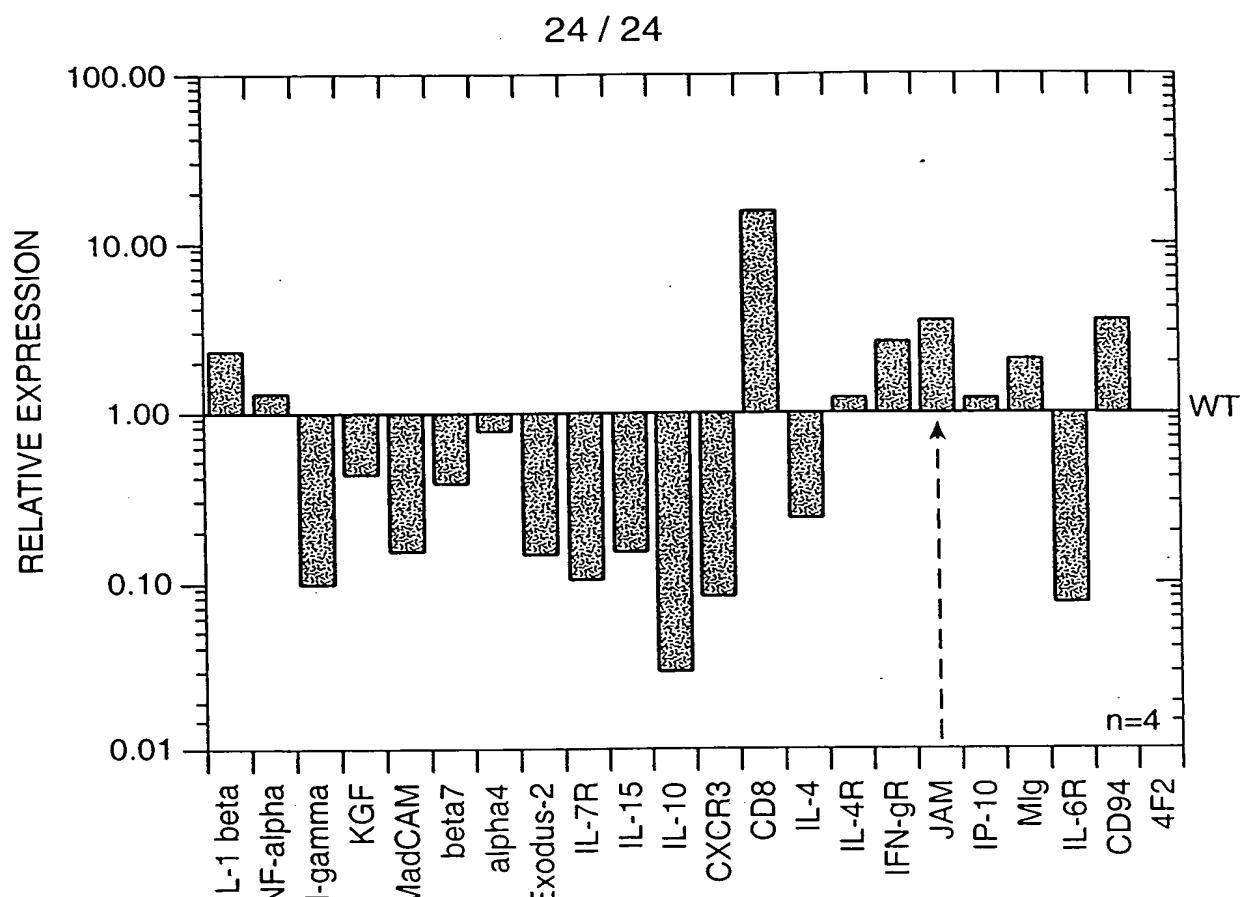
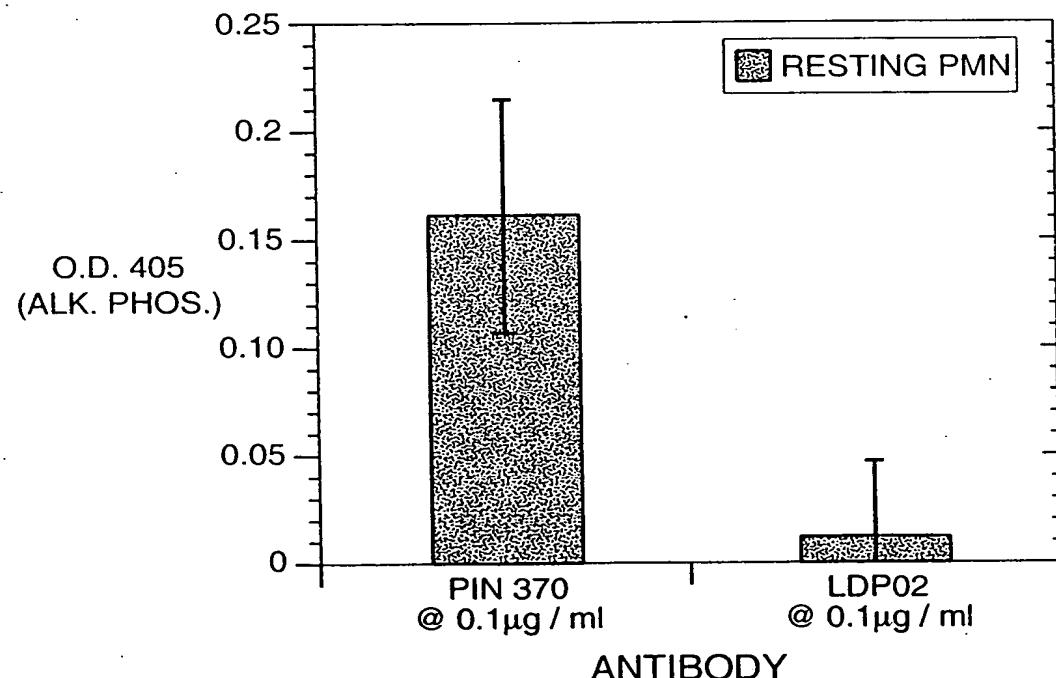
A33\_hum 238 Y Y . G I A V G V V A A L I I G I I Y C . . . . C C C C A G K D D N T E D A R P N R E A Y E E  
jam 235 N Y G G I I V A A V L V T L I I L G L L I F G V W F A Y S R G Y F E . I T K K G T A P G K K V I Y S Q

A33\_hum 284 P P E O L R E L S R E R E E E D O Y R Q E E Q R S T G R E S P D H L D Q  
jam 284 P S T A S E G E F K Q T S S F L V

<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>
WHOLE BRAIN	+	HEART	++	KIDNEY	+++
AMYGDALA	+	AORTA	+	LIVER	++
CAUDATE NUCLEUS	+	SKELETAL MUSCLE	+	SMALL INTESTINE	++
CEREBELLUM	-	COLON	+++	SPLEEN	++
CEREBRAL CORTEX	+	BLADDER	++	THYMUS	++
FRONTAL LOBE	+	UTERUS	+	PERIPHERAL LEUKOCYTE	+
HIPPOCAMPUS	+	PROSTATE	+++	LYMPH NODE	+
MEDULLA OBLONGATA	+	STOMACH	+++	BONE MARROW	+
OCCIPITAL LOBE	+	TESTIS	++	APPENDIX	+
PUTAMEN	+	OVARY	++	LUNG	++++
SUSTANTIA NIGRA	+	PANCREAS	++	TRACHEA	++++
TEMPORAL LOBE	+	PITUITARY GLAND	++	PLACENTA	++++
THalamus	+	ADRENAL GLAND	++		
NUCLEUS ACCUMBENS	+	THYROID GLAND	++	FETAL BRAIN	+
SPINAL CORD	-	SALIVARY GLAND	++	FETAL HEART	+
		MAMMARY GLAND	++	FETAL KIDNEY	++
				FETAL LIVER	++
				FETAL SPLEEN	+
				FETAL LUNG	++++

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FIG.- 19

**FIG.\_20****FIG.\_21**